

FIGURE 1

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[illegible]

FIGURE 2 A

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		250	
			TSLNPDYREE
PDGF-A	KVEVVRKKPK	LKEVQVRLEE	HLEACAT..
PDGF-B	KIEIVRKKPI	FKKATVTLED	HLACKCETVA
PlGF-1	KIRSG..DRP	.SYVELTFSQ	HVRCECRPLR
VEGF165	RIKPH..QGQ	.HIGEMSFLQ	HNKCECRPKK
VEGF-B167	MIRYP..SSQ	..LGEMSLEE	HSQCECRPKK
VEGF-C	EITVPLSQGP	.KPV ¹ TISFAN	HTSCRCMSKL
			DVYRQVHSII
			RRSLPATLPQ
		300	
		251	
PDGF-A	DTDVR.....
PDGF-B	QTRVTIRTVR	VRRPPKGKHR	KFKH ¹ THDKTA
PlGF-1MKPERCGDA
VEGF165ARQENPCGP
VEGF-B167	AVKPDSPRPL
VEGF-C	CQAANKTCPT	NYMWN ¹ NHICR	CLAQEDFMFS
			SDAGDDSTDG
			FHDICGPNKE
		301	
PDGF-A
PDGF-B
PlGF-1
VEGF165	QDPQ ¹ CKCSC	KNTDS.RCKA	RQELNERTC
VEGF-B167	PDPR ¹ TCRCRC	RRRSFLRCQG	RGLELNPDTC
VEGF-C	LDEETCQCVC	RAGLRPASC	PHKELDRNSC
			QCVCKNKLFP
			SQCGANREFD

FIGURE 2B

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	351		400
PDGF-A
PDGF-B
PlGF-1
VEGF165
VEGF-B167
VEGF-C	ENTCQCVCCKR TCPRNQPLNP GKCAECTES POKCLLKGGK FHHQTCSYR		
	401		434
PDGF-A
PDGF-B
PlGF-1
VEGF165
VEGF-B167
VEGF-C	RPCTNRQKAC EPGFSYSEEV CRCVPSYWKR PQMS		

FIGURE 2 C

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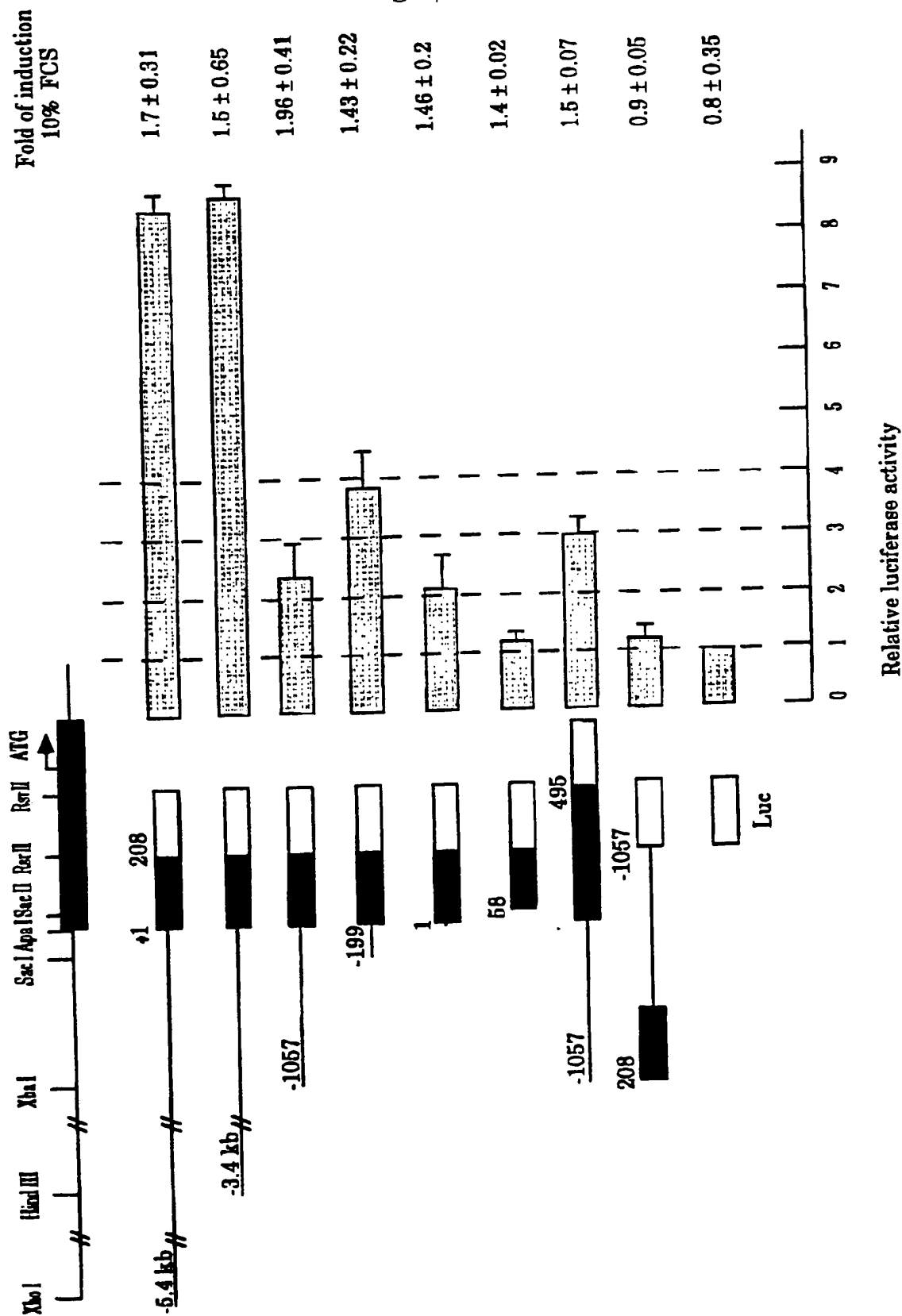


FIGURE 3

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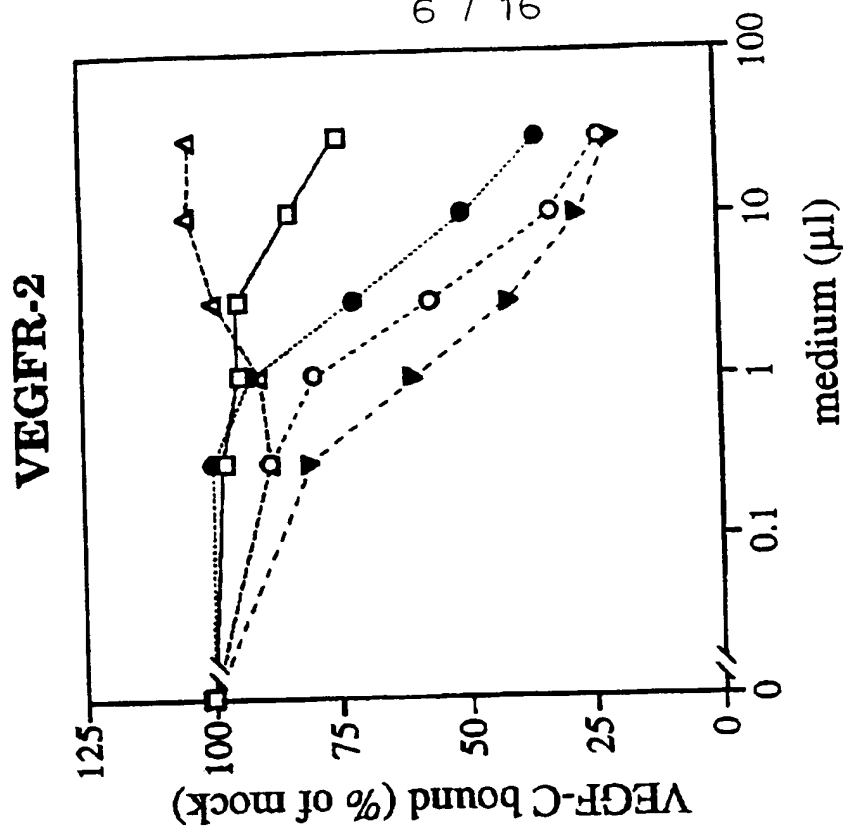


FIGURE 4B

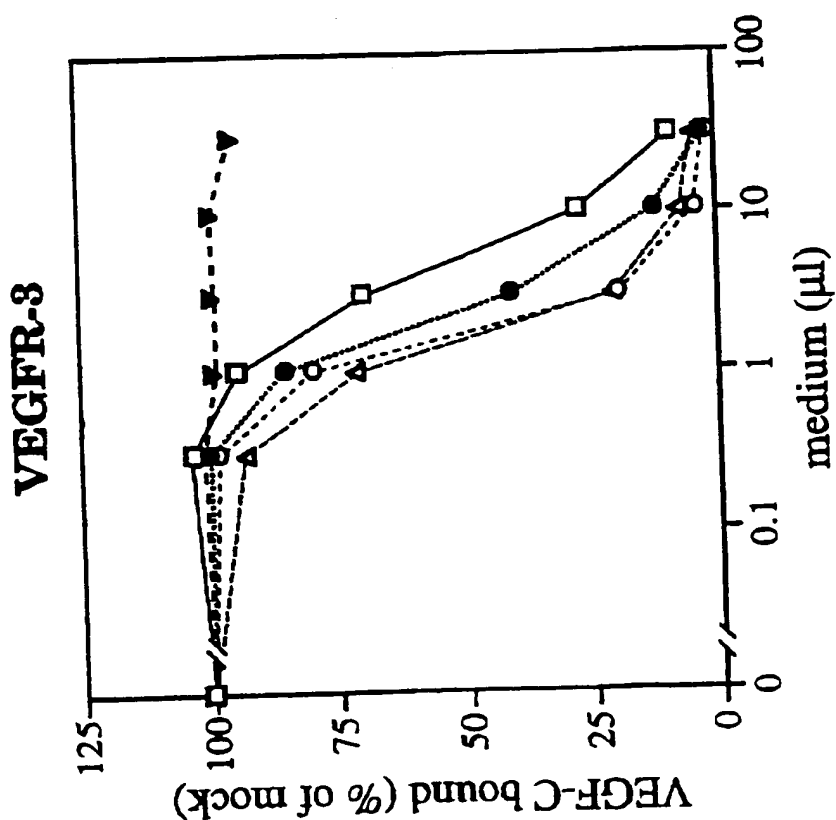


FIGURE 4A

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VEGF-C alignment

					50
	1				
Hum	BMLLGFFSVA	CSLLAAALLP	GPREAPAAAA	AFESGLDLSD	AEPDAGEATA
Mou	MHLLCFLSLA	CSLLAAALIP	SPREAPATVA	AFESGLGFSE	AEPDGGEVKA
Qua	MHLLLEMLSLG	CCLAAGAVLL	GPRQPPVA.A	AYESGHGYE	EEPGAGEPKA
					100
	51				
Hum	YASKDLEEQL	RSVSSVDELM	TVLYPEYWKM	YKCQLRKGGW	QHNREQANLN
Mou	FEGKDLEEQL	RSVSSVDELM	SVLYPDYWKM	YKCQLRKGGW	Q....QPTLN
Qua	HASKDLEEQL	RSVSSVDELM	TVLYPEYWKM	FKCQLRKGGW	QHNREHSSSD
					150
	101				
Hum	SRTEETIKFA	AAHYNTEILK	SIDNEWRTQ	CMPREVCIDV	GKEFGVATNT
Mou	TRTGDSVKFA	AAHYNTEILK	SIDNEWRTQ	CMPREVCIDV	GKEFGAATNT
Qua	TRSDDSLKFA	AAHYNAEILK	SIDTEWRKTQ	GMPREVCVDL	GKEFGATTNT
					200
	151				
Hum	FFKPPCVSVY	RCGGCCNSEG	LQCMNTTSTY	LSKTLFEITV	PLSQGPKPVT
Mou	FFKPPCVSVY	RCGGCCNSEG	LQCMNTSTGY	LSKTLFEITV	PLSQGPKPVT
Qua	FFKPPCVSIY	RCGGCCNSEG	LQCMNISTNY	ISKTLFEITV	PLSHGPKPVT
					250
	201				
Hum	ISFANHTSCR	CMSKLDVYRQ	VHSIIRSLP	ATLPQCOAAN	KTCPTNYMWN
Mou	ISFANHTSCR	CMSKLDVYRQ	VHSIIRSLP	ATLPQCOAAN	KTCPTNYVWN
Qua	VSFANHTSCR	CMSKLDVYRQ	VHSIIRSLP	ATQTQCHVAN	KTCPKNHVWN
					300
	251				
Hum	NHICRCLAQE	DFMFSSDAGD	DSTDGFHDIC	GPNKELDEET	CQCVCRAGLR
Mou	NYMCRCLAQQ	DFIFYSNVED	DSTNGFHDVC	GPNKELDEET	CQCVCCKGGLR
Qua	NQICRCLAQH	DFGFSSHLGD	SDTSEGFHIC	GPNKELDEET	CQCVCCKGGVR
					350
	301				
Hum	PASCGPHKEL	DRNSCQCVCK	NKLFPSCGA	NREFDENTCQ	CVCKRTCPRN
Mou	PSSCGPHKEL	DRDSCQCVCK	NKLFPNSCGA	NREFDENTCQ	CVCKRTCPRN
Qua	PISCGPHKEL	DRASCQCMCK	NKLLPSSCGP	NKEFDEEKQ	CVCKKTCPKH
					400
	351				
Hum	QPLNPGKCAC	ECTESPQKCL	LKGKKFHHQT	CSCYRRPCTN	RQKACEPGFS
Mou	QPLNPGKCAC	ECTENTQKCF	LKGKKFHHQT	CSCYRRPCAN	RLKHCDPGLS
Qua	HPLNPAKCIC	ECTESPNKCF	LKGKRFHHQT	CSCYRPPCTV	RTKRC DAGFL
					420
	401				
Hum	YSEEVCRCPV	SYWKRPMMS*			
Mou	FSEEVCRCPV	SYWKRPHLN.			
Qua	LAEEVCRCPV	TSWKRPLMN*			

FIGURE 5

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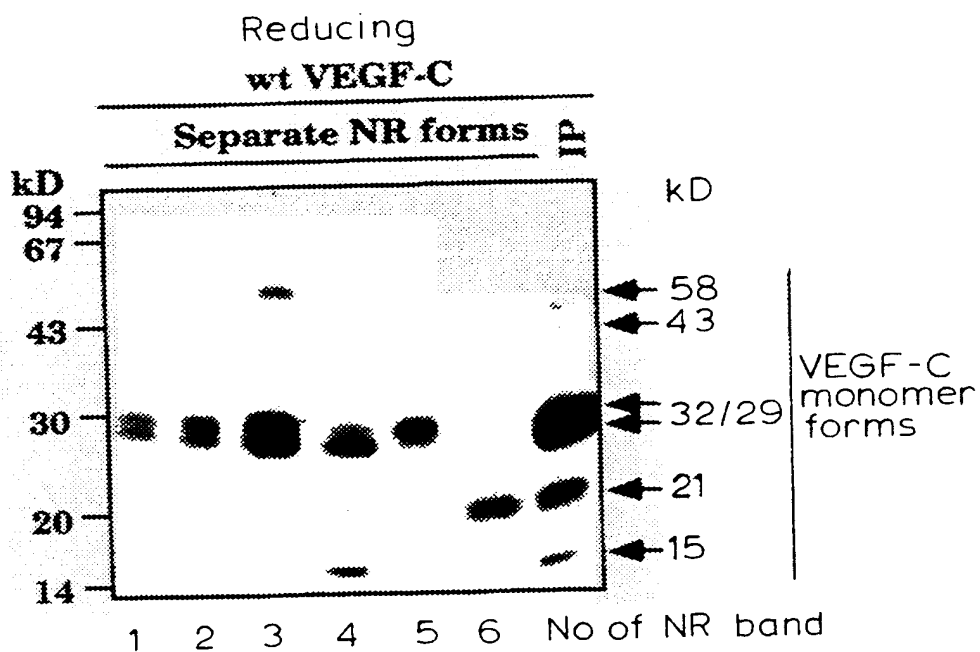


FIGURE 6A

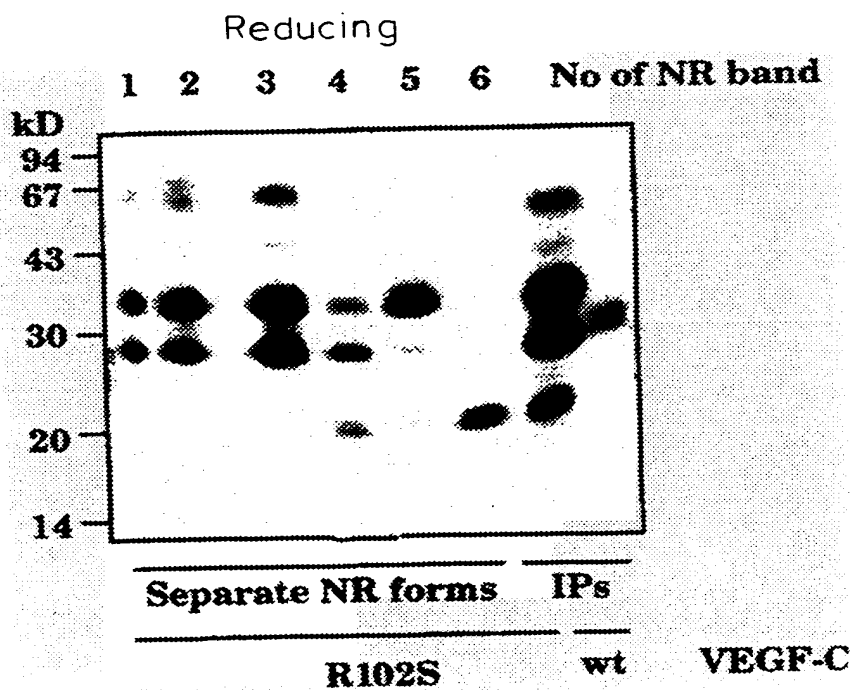
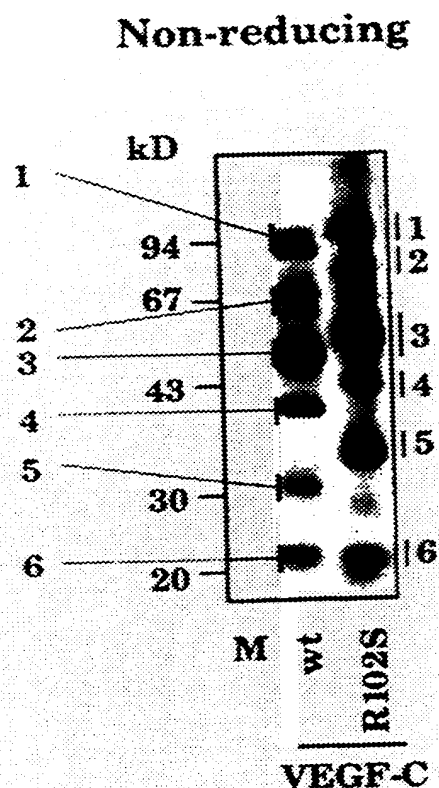


FIGURE 6C

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**FIGURE 6B**

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MEDIA

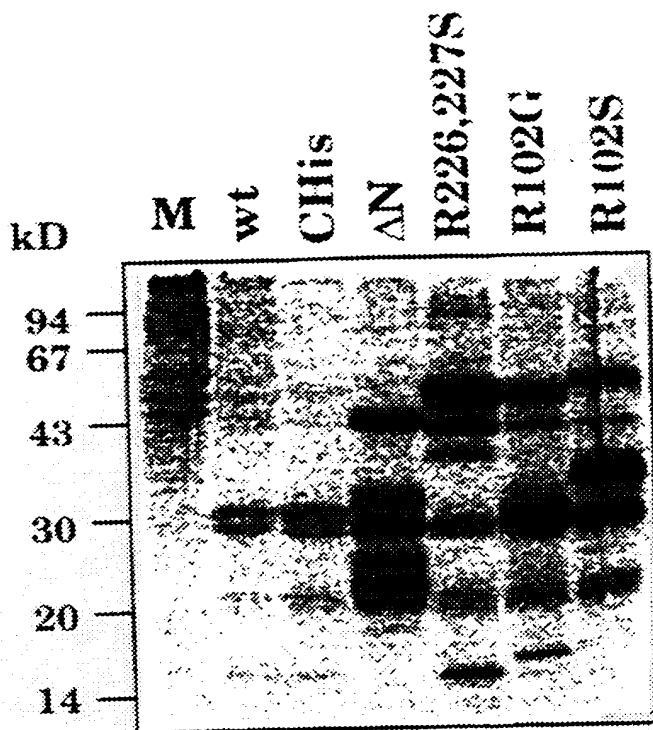


FIGURE 7A

LYSATES

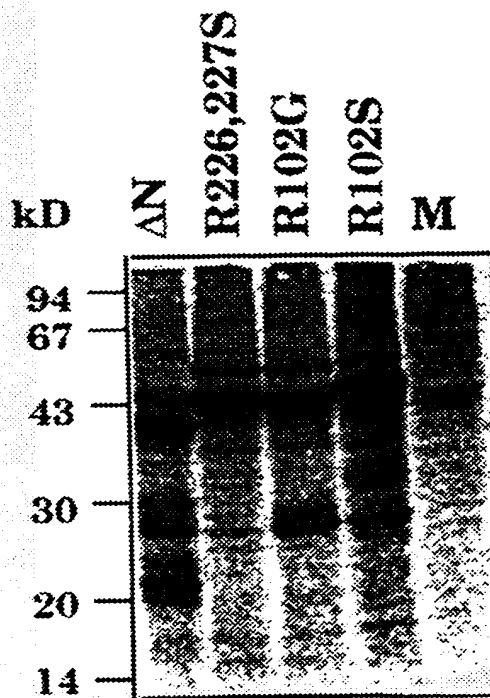


FIGURE 7B

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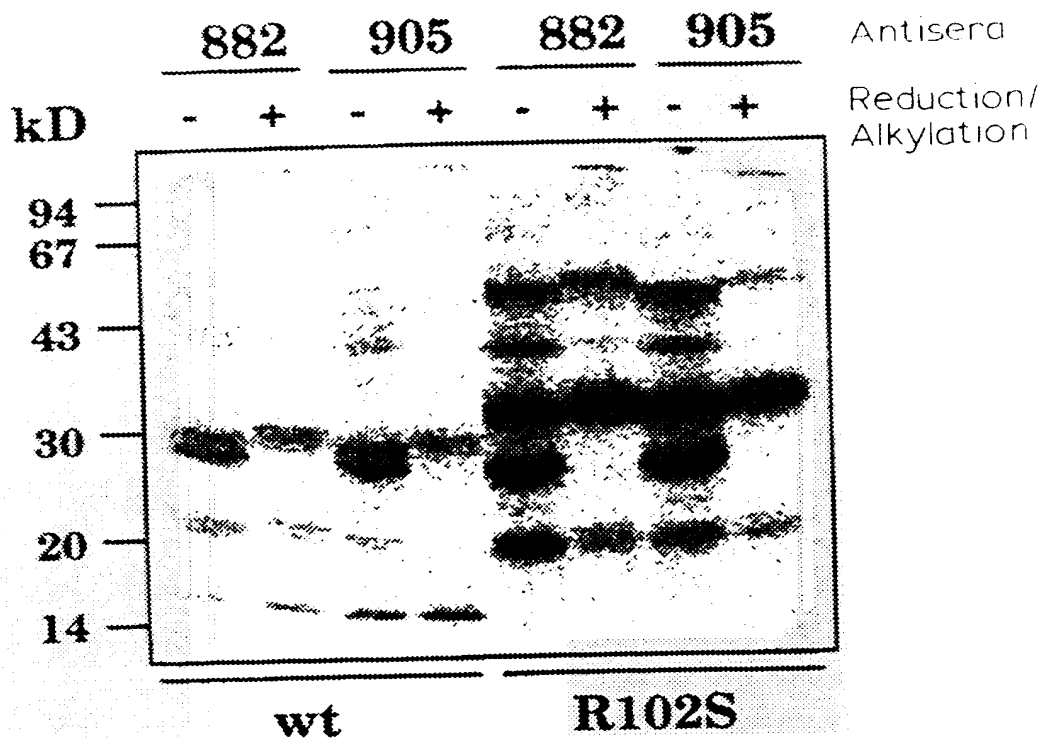


FIGURE 8A

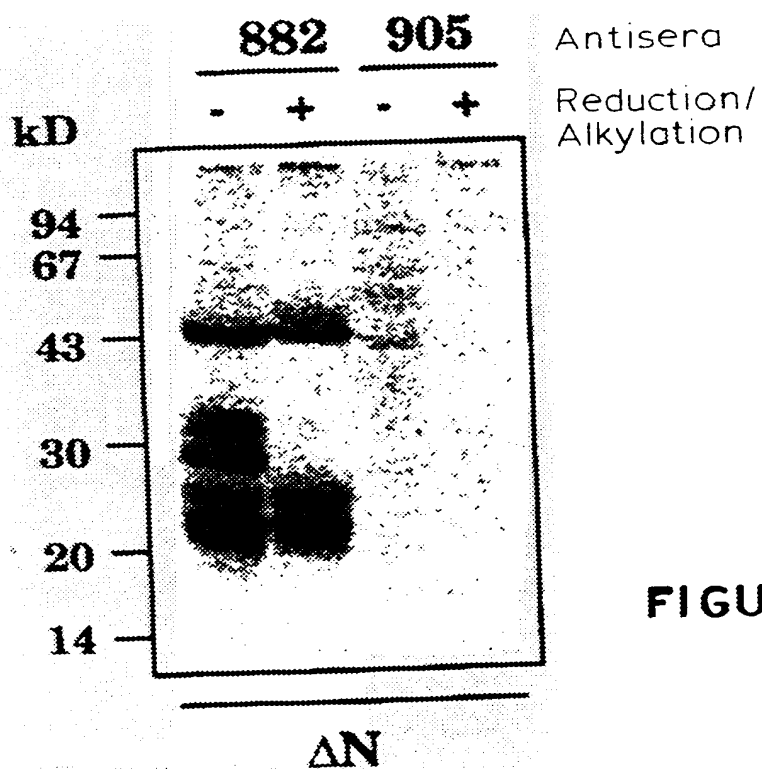


FIGURE 8B

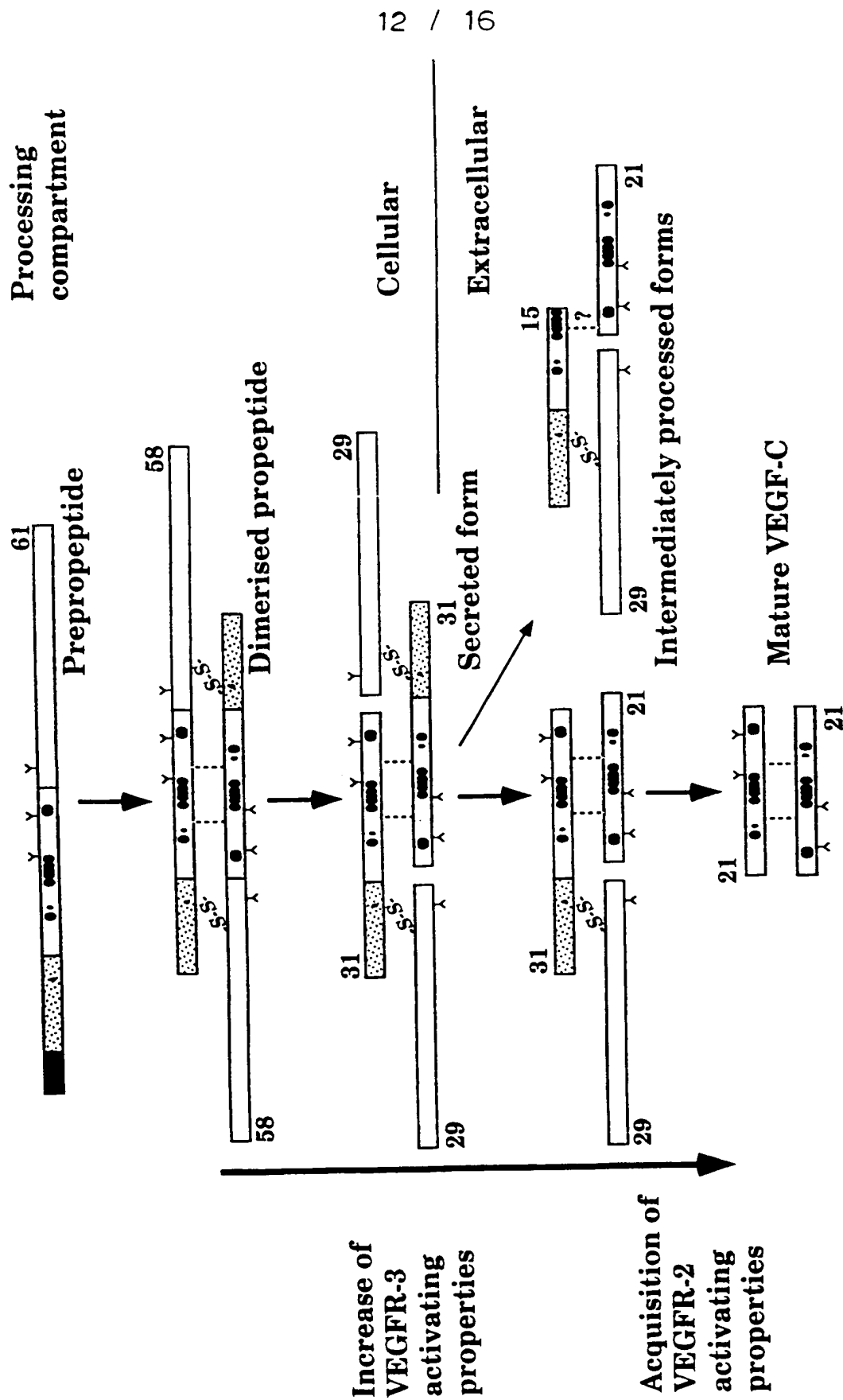


FIGURE 9

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HUMAN Exon length	Donor site	Intron length	Acceptor site
.....G...E...A...T(49).....A...Y...A...S.A...Y...A...S.
E1.....GGC.GAG.GCC.ACG.gtaggtctgcgt...>10.kb..TTTCTTTGACAG.GCT.TAT.GCA.AGC
.....E...I...L...K(116).....S...I...D...N.
E2.214.bp..GAG.ATC.TTG.AAA.Agtaagtatggg...1.6.kb...atgacttgacagGT.ATT.GAT.AAT
.....L...S...K...T(180).....L...F...E...I.
E3.191.bp..CTC.AGC.AAG.AAG.ACG.gtggtattgt.....9.kb.cccttcttcttag.TTA.TTT.GAA.ATTC...Q...A...A.
.....T...L...P...Q(231).....
E4.152.bp..ACA.CTA.CCA.Cagtgagtatgaattaa.>10.kb..ttctccaaagG.TGT.CAG.GCA.GCGD...S...T...D.
.....A...G...D... (266).....
E5.107.bp..GCT.GGA.GAT.Ggtagcagaatg.....301.bp...ctatttgtctagAC.TCA.ACA.GATC...Y...R...R.
.....Q...T...C...S(378).....
E6.334.bp..CAA.ACA.TGC.AGgtaagatcc.....>10.kb..tgttctcctagC.TGT.TAC.AGA.CGG
.....Q...M...S(419)Stop.....
E7.(501).bp..CAA.ATG.AGC.TAA.GTATGTACTGTT...ATTGTATTAT

FIGURE 11A

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MOUSE Exon length	Donor site	Intron length	Acceptor site
.....G...E...V...K(49).....A...F...E...G.			
E1.....GGC.GAG.GTC.AAG.gtaggtgaagg.>10.kb.attgtcttgacag.GCT.TTT.TGA.AGG			
.....E...I...L...K(116).....S...I...D...N.			
E2.201.bp..GAG.ATC.CTG.AAA.Agtaagtag.....4.kb....tgtgactcgacagGT.ATT.GAT.AAT			
.....L...S...K...T(180).....L...F...E...I.			
E3.191.bp..CTC.AGC.AAG.ACG.gtaggtat.....9.kb..ttgtccctttag.TTG.TTT.GAA.ATT			
.....T...L...P...Q(231).....C...Q...A...A.			
E4.152.bp..ACA.TTA.CCA.CAGtgagtatg.....10.kb.gtctcccccaaaagG.TGT.CAG.GCA.GCT			
.....N...V...E...D(266).....D...S...T...N.			
E5.107.bp..AAT.GTT.GAA.GAT.Ggtaagtaaaa...350.bp.....tctagAC.TCA.ACC.AAT			
.....Q...T...C...S(378).....C...Y...R...R.			
E6.334.bp..CAA.ACA.TGC.AGgtaaggagtg.....6.kb..ttttcccctagt.TGT.TAC.AGA.AGA			
.....H...L...N(415)Stop.....polyA.....			
E7.506.bp..CAT.CTG.AAC.TAA.GATCATACC...ATTGTATTATATAAgctgtgaag			

FIGURE 11B

